

10/049280

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SEQUENCE LISTING

<110> BASF Aktiengesellschaft

<120> Homogentisate-Dioxygenase

<130> M/40226

<140> 19937957.2

<141> 1999-08-11

<160> 15

<170> PatentIn Ver. 2.1

<210> 1

<211> 575

<212> DNA

<213> Brassica napus

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<221> misc_feature

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<223> /function= "restriction site"

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<222> (570)..(575)

<223> /function = "restriction site"

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gtgccttata agtatgacct gcacaagttc tgtccataca acactgtcct tgtagaccat 240
ggagatccat ctgtaaatac agttctgaca gcaccaacgg ataaacctgg tgtggccttg 300
cttgattttg tcatattccc tctcgtttgg ttggttgctg agcatacctt tcgacctcct 360
tactaccatc gtaactgcat gagtgaattt atgggcctaa tctatggtgc ttacgaggcc 420
aaagctgatg gatttctacc tgggtggcgca agtcttcaca gttgtatgac acctcatggt 480
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 <212> DNA
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<210> 10
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<223> /function = "restriction site"

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<222> (1154)..(1159)
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gct gat cct ttt cca gtt aag gga atg gat gct gtt gtt ttc gct gtt 97
Ala Asp Pro Phe Pro Val Lys Gly Met Asp Ala Val Val Phe Ala Val
15 20 25 30

gga aac gct aag caa gct gct cat tac tac tct act gct ttc gga atg 145
Gly Asn Ala Lys Gln Ala Ala His Tyr Tyr Ser Thr Ala Phe Gly Met
35 40 45

caa ctt gtt gct tac tct gga cca gaa aac gga tct aga gaa act gct 193
Gln Leu Val Ala Tyr Ser Gly Pro Glu Asn Gly Ser Arg Glu Thr Ala
50 55 60

tct tac gtt ctt act aac gga tct gct aga ttc gtt ctt act tct gtt 241

Ser	Tyr	Val	Leu	Thr	Asn	Gly	Ser	Ala	Arg	Phe	Val	Leu	Thr	Ser	Val	
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att	aag	cca	gct	acc	cca	tgg	gga	cat	ttc	ctt	gct	gat	cac	gtt	gct	289
Ile	Lys	Pro	Ala	Thr	Pro	Trp	Gly	His	Phe	Leu	Ala	Asp	His	Val	Ala	
	80					85					90					
gaa	cac	gga	gat	gga	gtt	gtt	gat	ctt	gct	att	gaa	gtt	cca	gat	gct	337
Glu	His	Gly	Asp	Gly	Val	Val	Asp	Leu	Ala	Ile	Glu	Val	Pro	Asp	Ala	
	95				100					105					110	
aga	gct	gct	cat	gct	tac	gct	att	gaa	cat	gga	gct	aga	tct	gtt	gct	385
Arg	Ala	Ala	His	Ala	Tyr	Ala	Ile	Glu	His	Gly	Ala	Arg	Ser	Val	Ala	
				115					120					125		
gaa	cca	tac	gaa	ctt	aag	gat	gaa	cat	gga	act	gtt	gtt	ctt	gct	gct	433
Glu	Pro	Tyr	Glu	Leu	Lys	Asp	Glu	His	Gly	Thr	Val	Val	Leu	Ala	Ala	
			130					135					140			
att	gct	act	tac	gga	aag	act	aga	cat	act	ctt	gtt	gat	aga	act	gga	481
Ile	Ala	Thr	Tyr	Gly	Lys	Thr	Arg	His	Thr	Leu	Val	Asp	Arg	Thr	Gly	
		145					150					155				
tac	gat	gga	cca	tac	ctt	cca	gga	tac	gtt	gct	gct	gct	cca	att	gtt	529
Tyr	Asp	Gly	Pro	Tyr	Leu	Pro	Gly	Tyr	Val	Ala	Ala	Ala	Pro	Ile	Val	
	160					165					170					
gaa	cca	cca	gct	cat	aga	acc	ttc	caa	gct	att	gac	cat	tgt	gtt	ggt	577
Glu	Pro	Pro	Ala	His	Arg	Thr	Phe	Gln	Ala	Ile	Asp	His	Cys	Val	Gly	
	175				180					185					190	
aac	gtt	gaa	ctc	gga	aga	atg	aac	gaa	tgg	gtt	gga	ttc	tac	aac	aag	625
Asn	Val	Glu	Leu	Gly	Arg	Met	Asn	Glu	Trp	Val	Gly	Phe	Tyr	Asn	Lys	
				195					200					205		
gtt	atg	gga	ttc	act	aac	atg	aag	gaa	ttc	gtt	gga	gat	gat	att	gct	673
Val	Met	Gly	Phe	Thr	Asn	Met	Lys	Glu	Phe	Val	Gly	Asp	Asp	Ile	Ala	
			210					215					220			
act	gag	tac	tct	gct	ctt	atg	tct	aag	gtt	gtt	gct	gat	gga	act	ctt	721
Thr	Glu	Tyr	Ser	Ala	Leu	Met	Ser	Lys	Val	Val	Ala	Asp	Gly	Thr	Leu	
		225					230					235				
aag	gtt	aaa	ttc	cca	att	aat	gaa	cca	gct	ctt	gct	aag	aag	aag	tct	769
Lys	Val	Lys	Phe	Pro	Ile	Asn	Glu	Pro	Ala	Leu	Ala	Lys	Lys	Lys	Ser	
	240					245					250					
cag	att	gat	gaa	tac	ctt	gag	ttc	tac	gga	gga	gct	gga	gtt	caa	cat	817
Gln	Ile	Asp	Glu	Tyr	Leu	Glu	Phe	Tyr	Gly	Gly	Ala	Gly	Val	Gln	His	
	255				260					265					270	
att	gct	ctt	aac	act	gga	gat	atc	gtg	gaa	act	gtt	aga	act	atg	aga	865
Ile	Ala	Leu	Asn	Thr	Gly	Asp	Ile	Val	Glu	Thr	Val	Arg	Thr	Met	Arg	
				275					280					285		
gct	gca	gga	gtt	caa	ttc	ctt	gat	act	cca	gat	tct	tac	tac	gat	act	913
Ala	Ala	Gly	Val	Gln	Phe	Leu	Asp	Thr	Pro	Asp	Ser	Tyr	Tyr	Asp	Thr	

290	295	300	
ctt ggt gaa tgg gtt gga gat act aga gtt cca gtt gat act ctt aga			961
Leu Gly Glu Trp Val Gly Asp Thr Arg Val Pro Val Asp Thr Leu Arg			
305	310	315	
gaa ctt aag att ctt gct gat aga gat gaa gat gga tac ctt ctt caa			1009
Glu Leu Lys Ile Leu Ala Asp Arg Asp Glu Asp Gly Tyr Leu Leu Gln			
320	325	330	
atc ttc act aag cca gtt caa gat aga cca act gtg ttc ttc gaa atc			1057
Ile Phe Thr Lys Pro Val Gln Asp Arg Pro Thr Val Phe Phe Glu Ile			
335	340	345	350
att gaa aga cat gga tct atg gga ttc gga aag ggt aac ttc aag gct			1105
Ile Glu Arg His Gly Ser Met Gly Phe Gly Lys Gly Asn Phe Lys Ala			
355	360	365	
ctt ttc gaa gct att gaa aga gaa caa gag aag aga gga aac ctt tag			1153
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<220>
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 35 40 45
 Val Ala Tyr Ser Gly Pro Glu Asn Gly Ser Arg Glu Thr Ala Ser Tyr
 50 55 60
 Val Leu Thr Asn Gly Ser Ala Arg Phe Val Leu Thr Ser Val Ile Lys
 65 70 75 80
 Pro Ala Thr Pro Trp Gly His Phe Leu Ala Asp His Val Ala Glu His
 85 90 95
 Gly Asp Gly Val Val Asp Leu Ala Ile Glu Val Pro Asp Ala Arg Ala
 100 105 110
 Ala His Ala Tyr Ala Ile Glu His Gly Ala Arg Ser Val Ala Glu Pro

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Tyr	Glu	Leu	Lys	Asp	Glu	His	Gly	Thr	Val	Val	Leu	Ala	Ala	Ile	Ala
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Thr	Tyr	Gly	Lys	Thr	Arg	His	Thr	Leu	Val	Asp	Arg	Thr	Gly	Tyr	Asp
145					150					155					160
Gly	Pro	Tyr	Leu	Pro	Gly	Tyr	Val	Ala	Ala	Ala	Pro	Ile	Val	Glu	Pro
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Pro	Ala	His	Arg	Thr	Phe	Gln	Ala	Ile	Asp	His	Cys	Val	Gly	Asn	Val
			180					185					190		
Glu	Leu	Gly	Arg	Met	Asn	Glu	Trp	Val	Gly	Phe	Tyr	Asn	Lys	Val	Met
			195				200					205			
Gly	Phe	Thr	Asn	Met	Lys	Glu	Phe	Val	Gly	Asp	Asp	Ile	Ala	Thr	Glu
	210					215					220				
Tyr	Ser	Ala	Leu	Met	Ser	Lys	Val	Val	Ala	Asp	Gly	Thr	Leu	Lys	Val
225					230					235					240
Lys	Phe	Pro	Ile	Asn	Glu	Pro	Ala	Leu	Ala	Lys	Lys	Lys	Ser	Gln	Ile
			245					250						255	
Asp	Glu	Tyr	Leu	Glu	Phe	Tyr	Gly	Gly	Ala	Gly	Val	Gln	His	Ile	Ala
			260					265					270		
Leu	Asn	Thr	Gly	Asp	Ile	Val	Glu	Thr	Val	Arg	Thr	Met	Arg	Ala	Ala
			275				280					285			
Gly	Val	Gln	Phe	Leu	Asp	Thr	Pro	Asp	Ser	Tyr	Tyr	Asp	Thr	Leu	Gly
	290					295					300				
Glu	Trp	Val	Gly	Asp	Thr	Arg	Val	Pro	Val	Asp	Thr	Leu	Arg	Glu	Leu
305					310					315				320	
Lys	Ile	Leu	Ala	Asp	Arg	Asp	Glu	Asp	Gly	Tyr	Leu	Leu	Gln	Ile	Phe
			325						330					335	
Thr	Lys	Pro	Val	Gln	Asp	Arg	Pro	Thr	Val	Phe	Phe	Glu	Ile	Ile	Glu
			340					345					350		
Arg	His	Gly	Ser	Met	Gly	Phe	Gly	Lys	Gly	Asn	Phe	Lys	Ala	Leu	Phe
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Glu	Ala	Ile	Glu	Arg	Glu	Gln	Glu	Lys	Arg	Gly	Asn	Leu			
	370					375					380				